

Fig. 1. Schematic diagram of methoxy mycolic acid synthase *mmaA* 4-*mmaA* 1 gene cluster of mycobacteria and location of forward A, and reverse D primers.

CTACTTCGCCAGCGTGAACTGGTTGACGTCGATGTAGCCGACCCGGAACAGCTTGGCGCAGCCGGTCA
GGTATTTTCATGTACCGCTCGTAGACCTCTTCGGACTGGATCGCGATGGCCTCGCTTTTGTGTTCTGCA
GCGCCTCGGCCCACAGGTCGAGGGTCCTGGCGTAATGCGGCTGCAGCGACTGGCGGCGAGTCAGCGT
GAAACCCGTCTTCGCCGACTGTTCTCAACCATTTCAATCGTCGGAGGTTGGCCCCCGGGAAGATTTG
GGTCGCGATGAACTTGAGAAAGCGGGCCAGCCACAACGTGAGCGGCAAGCCGTGGTTCGACCATCTGC
TGCCTGGTCAGGCCGGTGATCGTGTGCAGCAGCAACACGCCATCGGGCGGCAGGATTTTGTGGGCCCC
GGCGAAGAAGTCGGCGTGACGATCGTGGCCGAAGTGCTCGAACGCGCCGATCGACACGATGCGGTGCG
ACGGGCTCGTTGAACTGCTCCCATCCCGCCAGCAACACTCGCCTGTCGCGCGGGGTGTCCATCTCGTGC
AACGACTTCTGCACATGGGCGGCCTGGTTCTTCGACAATGTCAGGCCGACGACGTTGACGTCATACTG
CGCGATCGCGCGCCGCATGGTGGCGCCCCAGCCGCAACCGATATCGAGCAGCGTCATGCCGGGCTGCA
GACCTAGCTTGCCAGCGCCAGGTCGATCTTGGCGATCTGGGCCTCTTCCAGCGTCATGTCCTCGCGTT
CGAAATGCGCGCAGCTGTAGGTCTGGGTGCGATCCAGGAACAGCCGGAAGAAGTCGTCGGACAGGTC
GTAGTGTGCCTGCACGTCCTCGAAGTGCGGCGTTAGGTCT*GTTGACCATgagggtgaatgcctttccggaccctaggtggcct*
ttcgggtcctgcaggaacgcaccgatgcttccccctcccccatgctcgaggcatgctatccgatacagggccgcccactaaaccgcatgaatttcccagggtca
*gggaacggatatgagcggacgagCTACTTGGTCATGGTGAAC*TGGGCGACGTTGATTAGGCCTCTGCGGAAGCGCT
CCGCGCATCCGGTCAGATAGTGCATGAAGTTGTTGTAGACCTCTTCGGACTGTACGGCGATGGCGCGT
TCGCGGGCAGCCTGTAGGTTGGCGGCCCATGCATC*GAGAGTCCGTGCGTAGTG*CTGCTGCAGCAGCTGG
ACATGCTCGATGGTGAAGCCCCGCGGCCTGCGCATTGTGCGACAATGTCGGGCTCCGATGGCAGCTCGCC
GCCCCGGAAGATCGACTCCCGCAGGAATTTGAGGAATCGAAGGTGCTCATCGTCAGCGCAATGCCCT
GTTTCGTGCAGCCACCTGCGGTGCTAGGTGAACAGGCTGTGCAGTAGCATCCGCCCCGTCATCGGGCAGG
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GACGATCCGGTCGACGTTCTCTTCAAACCTCTTCCCAGCCCTGCAGCCGGGCCCTCGGCGCGCCGTTGCGT
TCCGATTGCGGCCAGGCGGTCTTTGCTGCGTTCATAGTGATTCCGGCTGAGCGTGAGGCCGATGACATT
GACGTCGTACTTCTCCACGGCCCCGAACGAGCGCCCCGCCACCCGCAACCCACGTCGAGTAGCGTCA
TCCCCGGTTCGAGGTTTCACTTGTCCAACGCCAGATCCACCTTGCCAGTTGCGCCTCTTCCAGCGTCA
TATCGTCACGCTCGAAATAGGCGCAGGTGTAGACCCAGGTGGGATCGAGGAACAACGCGAAGAAGTC
ATCCGAAATGTCGTAAGCCGACTGTGACTCTTCGTAATATGGTCTCAGCTTGGCCAT

Fig. 2. Sequence of *mmaA2* and *mmaA1* gene with an intergenic region of 166 base pair (shown in lower case. Location of forward A, sequence ID 1 and reverse primer D, sequence ID 2. Both primer sequences are underlined and italicized.

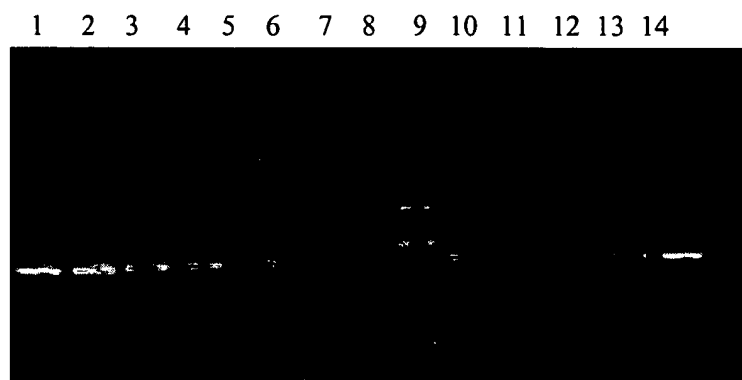


Fig. 3. PCR amplification of different mycobacterial genomic DNAs with primers A and D (lanes 1- 15): 1. *M.avium* 2. *M.bovis* 3. *M.chelonae* 4. *M.fortuitum* 5. *M.intracellulare* 6. *M.kansassi* 7. *M.phlei* 8. 100 bp DNA ladder 9. *M.marinum* 10. *M.scrofulaceum* 11.*M.smegmatis* 12. *M.szulgai*, 13. *M.tuberculosis* and 14. negative control. AD indicates 363 bp-amplified product.

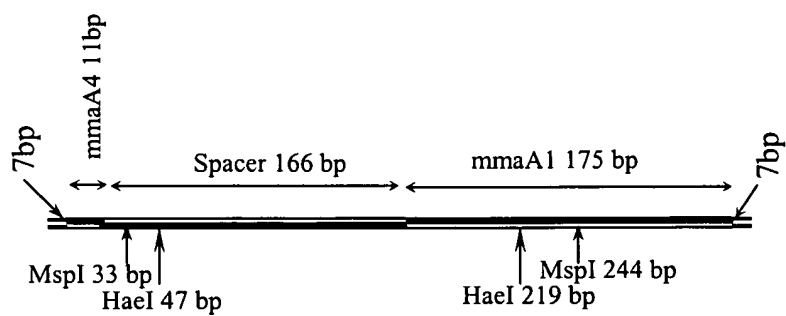


Fig. 4. Line diagram showing restriction endonuclease map of HaeI and MspI within AD.

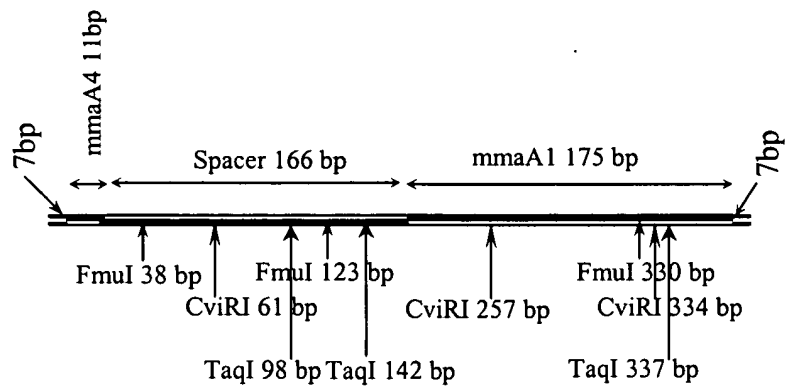


Fig. 5. Line diagram showing restriction endonuclease map of FmuI, CviRI and TaqI within AD.

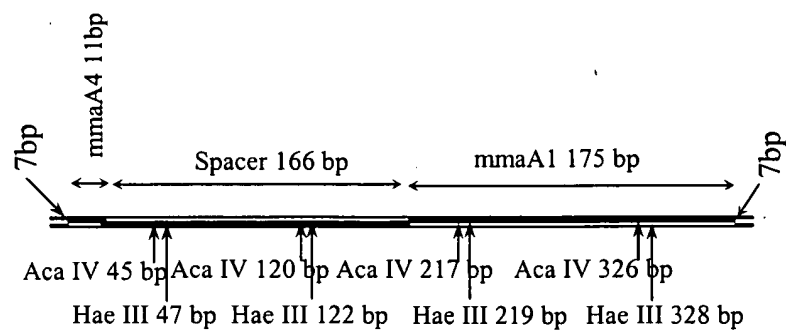


Fig. 6. Restriction map of AD showing distribution of the sites of restriction endonucleases AcaIV and HaeIII.

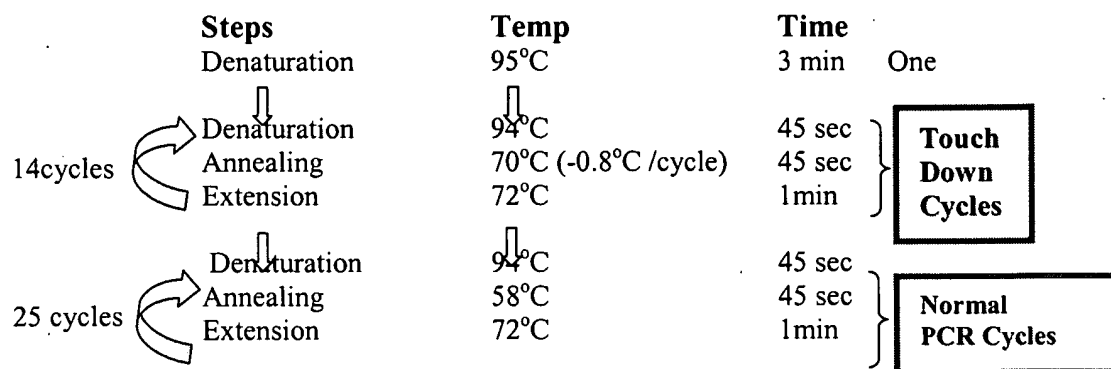


Fig. 7. Line diagram showing different steps of PCR reaction